



IFW16

RAW SEQUENCE LISTING

DATE: 07/27/2004

PATENT APPLICATION: US/09/303,232C

TIME: 11:45:23

Input Set : A:\Mo5176new_rev.txt

Output Set: N:\CRF4\07272004\I303232C.raw

2 <110> APPLICANT: Bayer Aktiengesellschaft
 4 <120> TITLE OF INVENTION: Nucleic Acids which encode
 5 insect acetylcholine receptor subunits
 7 <130> FILE REFERENCE: Le A 33 020-Foreign Countries
 9 <140> CURRENT APPLICATION NUMBER: US/09/303,232C
 10 <141> CURRENT FILING DATE: 1999-04-30
 12 <150> PRIOR APPLICATION NUMBER: DE 198 19 829.9
 13 <151> PRIOR FILING DATE: 1998-05-04
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2886
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Drosophila melanogaster
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 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (372)..(2681)
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 31 aaaacgctct tcgggttgta aagaaaataa gaagacaaaa gaaagacatg aaaacgttgc 120
 33 aaacaataaa gcatatactt gccatattga tataaaggga aatcgtgaaa aggcggtgaa 180
 35 aatttcgtaa gattagttgg tattaagggc agcccatgca cacagctaaa aagggaacta 240
 37 aaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300
 39 aattatatta ttgtaactta gtagagagca gacaacatat ccgctggcaa caaccaacac 360
 41 cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410
 42 Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp
 43 1 5 10
 45 gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458
 46 Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
 47 15 20 25
 49 agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506
 50 Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn
 51 30 35 40 45
 53 cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554
 54 Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
 55 50 55 60
 57 agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602
 58 Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala
 59 65 70 75
 61 tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650
 62 Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln
 63 80 85 90
 65 acg cat ctg caa cag cta gac agc agc aac atg ttg tcg cca aag aca 698



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66 Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr
67      95      100      105
69 gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca 746
70 Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro
71 110      115      120      125
73 aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga 794
74 Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg
75      130      135      140
77 cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa 842
78 Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln
79      145      150      155
81 cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc 890
82 Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr
83      160      165      170
85 tac agc aca cca gca gca aca acc agc tgt ccg aca gcc acc tac atg 938
86 Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met
87      175      180      185
89 caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat 986
90 Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His
91 190      195      200      205
93 gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag 1034
94 Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln
95      210      215      220
97 gtg ctg ctc gtg tcg ctg caa cag tgg caa ctt cac gtg caa cag cga 1082
98 Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg
99      225      230      235
101 tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att 1130
102 Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile
103      240      245      250
105 tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc 1178
106 Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser
107      255      260      265
109 agt agc agc agc aac agc agc aac aac agc agc acg caa ata tta aac 1226
110 Ser Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn
111 270      275      280      285
113 gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta 1274
114 Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu
115      290      295      300
117 tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac 1322
118 Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His
119      305      310      315
121 gat ctt ttg gat cct tat aat aca cta gaa cgt ccc gtt ctc aat gaa 1370
122 Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu
123      320      325      330
125 tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc 1418
126 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
127      335      340      345
129 gat gtg gac gag aaa aat caa ttg cta gtc act aat gtg tgg tta aaa 1466
130 Asp Val Asp Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys

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134	Leu	Glu	Trp	Asn	Asp	Met	Asn	Leu	Arg	Trp	Asn	Thr	Ser	Asp	Tyr	Gly	
135						370				375				380			
137	gga	gtt	aag	gat	ctg	cga	ata	ccg	ccg	cat	cgc	atc	tgg	aag	ccg	gac	1562
138	Gly	Val	Lys	Asp	Leu	Arg	Ile	Pro	Pro	His	Arg	Ile	Trp	Lys	Pro	Asp	
139						385				390				395			
141	gtg	ctg	atg	tac	aac	agt	gcg	gat	gag	gga	ttt	gac	ggc	acc	tac	cag	1610
142	Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Gly	Thr	Tyr	Gln	
143						400				405				410			
145	acg	aac	gtg	gtg	gtg	cgg	aac	aac	ggc	tcg	tgt	cta	tac	gtt	ccg	ccg	1658
146	Thr	Asn	Val	Val	Val	Arg	Asn	Asn	Gly	Ser	Cys	Leu	Tyr	Val	Pro	Pro	
147						415				420				425			
149	ggg	atc	ttc	aag	tcg	acg	tgc	aag	atc	gac	atc	acg	tgg	ttc	ccc	ttc	1706
150	Gly	Ile	Phe	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	
151	430					435				440				445			
153	gat	gac	cag	cgg	tgc	gag	atg	aag	ttc	ggc	agt	tgg	acc	tac	gac	gga	1754
154	Asp	Asp	Gln	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	
155						450				455				460			
157	ttc	cag	ctg	gat	tta	caa	tta	caa	gat	gaa	act	ggc	ggt	gat	atc	agc	1802
158	Phe	Gln	Leu	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Thr	Gly	Gly	Asp	Ile	Ser	
159						465				470				475			
161	agt	tac	gtg	ctc	aac	ggc	gag	tgg	gaa	cta	ctg	ggt	gtg	ccc	ggc	aaa	1850
162	Ser	Tyr	Val	Leu	Asn	Gly	Glu	Trp	Glu	Leu	Leu	Gly	Val	Pro	Gly	Lys	
163						480				485				490			
165	cgt	aac	gag	atc	tat	tac	aac	tgc	tgc	ccg	gaa	ccc	tat	ata	gac	atc	1898
166	Arg	Asn	Glu	Ile	Tyr	Tyr	Asn	Cys	Cys	Pro	Glu	Pro	Tyr	Ile	Asp	Ile	
167						495				500				505			
169	acc	ttc	gcc	atc	atc	atc	cgc	cga	cga	aca	ctg	tac	tat	ttc	ttc	aac	1946
170	Thr	Phe	Ala	Ile	Ile	Ile	Arg	Arg	Arg	Thr	Leu	Tyr	Tyr	Phe	Phe	Asn	
171	510					515				520				525			
173	ctg	atc	ata	cct	tgt	gta	ctg	att	gcc	tcc	atg	gcc	ttg	ctc	gga	ttc	1994
174	Leu	Ile	Ile	Pro	Cys	Val	Leu	Ile	Ala	Ser	Met	Ala	Leu	Leu	Gly	Phe	
175						530				535				540			
177	acc	ctg	ccg	cca	gat	tcg	ggt	gaa	aaa	tta	tcg	ctg	ggt	gtt	acc	atc	2042
178	Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Ser	Leu	Gly	Val	Thr	Ile	
179						545				550				555			
181	ttg	ctc	tcg	ctg	acc	gtg	ttt	ctg	aat	atg	gtt	gcc	gag	aca	atg	ccg	2090
182	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Asn	Met	Val	Ala	Glu	Thr	Met	Pro	
183						560				565				570			
185	gct	act	tcc	gat	gcg	gtg	cca	ttg	tgg	ata	cgc	atc	gtg	ttt	ttg	tgc	2138
186	Ala	Thr	Ser	Asp	Ala	Val	Pro	Leu	Trp	Ile	Arg	Ile	Val	Phe	Leu	Cys	
187						575				580				585			
189	tgg	ctg	cca	tgg	ata	ttg	cga	atg	agt	cgc	cca	gga	cga	ccg	ctg	atc	2186
190	Trp	Leu	Pro	Trp	Ile	Leu	Arg	Met	Ser	Arg	Pro	Gly	Arg	Pro	Leu	Ile	
191	590					595				600				605			
193	cta	gag	ttc	ccg	acc	acg	ccc	tgt	tcg	gac	aca	tcc	tcc	gag	cgg	aag	2234
194	Leu	Glu	Phe	Pro	Thr	Thr	Pro	Cys	Ser	Asp	Thr	Ser	Ser	Glu	Arg	Lys	
195						610				615				620			

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201 ctg ctg gcc aac gta cta gac atc gat gat gac ttc cgg cac aat tgt 2330
202 Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys
203          640          645          650
205 cgc ccc atg acg ccc ggc gga aca ctg cca cac aac ccg gct ttc tat 2378
206 Arg Pro Met Thr Pro Gly Gly Thr Leu Pro His Asn Pro Ala Phe Tyr
207          655          660          665
209 cgc acg gtt tat gga caa ggc gac gat ggc agc att ggg cca att ggc 2426
210 Arg Thr Val Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly
211 670          675          680          685
213 agc acc cga atg ccg gat gcg gtc acc cat acg tgc atc aaa tca 2474
214 Ser Thr Arg Met Pro Asp Ala Val Thr His His Thr Cys Ile Lys Ser
215          690          695          700
217 tca act gaa tat gaa tta ggt tta atc tta aag gaa att cgc ttt ata 2522
218 Ser Thr Glu Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile
219          705          710          715
221 act gat cag cta cgt aaa gat gac gag tgc aat gac att gcc aat gat 2570
222 Thr Asp Gln Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp
223          720          725          730
225 tgg aaa ttt gca gct atg gtc gtt gac aga ctg tgc ctt atc ata ttc 2618
226 Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe
227          735          740          745
229 aca atg ttc gca ata tta gcc aca ata gct gta cta cta tcg gca cca 2666
230 Thr Met Phe Ala Ile Leu Ala Thr Ile Ala Val Leu Leu Ser Ala Pro
231 750          755          760          765
233 cat att att gtc tcg tagccatg ggcgaggtgg ttattgttat tggttttatt 2721
234 His Ile Ile Val Ser
235          770
237 ataaaaatcaa tttgttaatt attaaattaa taacgaaact ctttaagtaa attaaaaacta 2781
239 aaaagacact aaaaaagcac aaaaaaatag gaaaatacat gataaaaccc atgaactaaa 2841
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246 <212> TYPE: PRT
247 <213> ORGANISM: Drosophila melanogaster
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254          20          25          30
256 Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn Gln Gln Leu
257          35          40          45
259 Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His Ser Asn Ile
260          50          55          60
262 Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala Ser Lys Asp
263 65          70          75          80
265 Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu

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266				85				90				95				
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272				115					120					125		
274	Arg	Leu	Cys	Ala	Arg	Lys	Arg	Gln	Arg	Leu	Arg	Arg	Arg	Arg	Lys	Arg
275				130					135					140		
277	Lys	Pro	Ala	Thr	Pro	Asn	Glu	Thr	Asp	Ile	Lys	Lys	Gln	Gln	Gln	Leu
278	145						150				155					160
280	Ser	Met	Pro	Pro	Phe	Lys	Thr	Arg	Lys	Ser	Thr	Asp	Thr	Tyr	Ser	Thr
281					165					170					175	
283	Pro	Ala	Ala	Thr	Thr	Ser	Cys	Pro	Thr	Ala	Thr	Tyr	Met	Gln	Cys	Arg
284				180					185					190		
286	Ala	Ser	Asp	Asn	Glu	Phe	Ser	Ile	Pro	Ile	Ser	Arg	His	Asp	Arg	Val
287				195				200					205			
289	Ser	Thr	Ala	Thr	Phe	Ala	Trp	Val	Leu	His	Val	Leu	Gln	Val	Leu	Leu
290				210				215				220				
292	Val	Ser	Leu	Gln	Gln	Trp	Gln	Leu	His	Val	Gln	Gln	Arg	Ser	Val	Leu
293	225						230				235					240
295	Leu	Phe	Arg	Arg	Ile	Ala	Ala	Ser	Thr	Ile	Ala	Phe	Ile	Ser	Tyr	Leu
296					245					250					255	
298	Gly	Ser	Phe	Ala	Ala	Gln	Leu	Lys	Asn	Ser	Ser	Ser	Ser	Ser	Ser	Ser
299				260					265					270		
301	Ser	Asn	Ser	Ser	Asn	Asn	Ser	Ser	Thr	Gln	Ile	Leu	Asn	Gly	Leu	Asn
302				275					280					285		
304	Lys	His	Ser	Trp	Ile	Phe	Leu	Leu	Ile	Tyr	Leu	Asn	Leu	Ser	Ala	Lys
305				290				295				300				
307	Val	Cys	Leu	Ala	Gly	Tyr	His	Glu	Lys	Arg	Leu	Leu	His	Asp	Leu	Leu
308	305						310				315					320
310	Asp	Pro	Tyr	Asn	Thr	Leu	Glu	Arg	Pro	Val	Leu	Asn	Glu	Ser	Asp	Pro
311					325					330					335	
313	Leu	Gln	Leu	Ser	Phe	Gly	Leu	Thr	Leu	Met	Gln	Ile	Ile	Asp	Val	Asp
314				340					345					350		
316	Glu	Lys	Asn	Gln	Leu	Leu	Val	Thr	Asn	Val	Trp	Leu	Lys	Leu	Glu	Trp
317				355				360					365			
319	Asn	Asp	Met	Asn	Leu	Arg	Trp	Asn	Thr	Ser	Asp	Tyr	Gly	Gly	Val	Lys
320				370				375				380				
322	Asp	Leu	Arg	Ile	Pro	Pro	His	Arg	Ile	Trp	Lys	Pro	Asp	Val	Leu	Met
323	385						390				395					400
325	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Gly	Thr	Tyr	Gln	Thr	Asn	Val
326				405						410					415	
328	Val	Val	Arg	Asn	Asn	Gly	Ser	Cys	Leu	Tyr	Val	Pro	Pro	Gly	Ile	Phe
329				420					425					430		
331	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	Asp	Asp	Gln
332				435					440				445			
334	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	Phe	Gln	Leu
335				450			455				460					
337	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Thr	Gly	Gly	Asp	Ile	Ser	Ser	Tyr	Val
338	465					470				475						480

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 6
Seq#:8; N Pos. 9

VERIFICATION SUMMARY

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L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0